

OSIRIS Release Notes Version 2.13.1

OSIRIS Version 2.13.1 is a bug fix version

Bug Fix:

- Corrected the version data in kit Operating Procedures that prevented them from being saved as a custom Operating Procedure with changes to the lab settings in OSIRIS version 2.13. The following Operating Procedures that could not be modified in version 2.13 will function normally in version 2.13.1. This change has no impact on the accuracy or results of analysis in OSIRIS beyond the ability to use these Operating Procedures.

[IdentifilerPlus w/o ILS @250]

[NGMSElect]

[SEfilerPlus]

Improvements in OSIRIS Version 2.13

Version 2.13 includes substantial improvements over previous versions

New Features

Fragment Analysis

Version 2.13 introduces the functionality for users to do size-base fragment analysis without the need of an allelic ladder, needing only an internal size marker in the sample. Included are Lab Settings that allow analysis of 2, 3, 4, and 5 channel analyses, and settings to allow users to designate the channel in which the marker data resides. This allows users to analyze home-made multiplexes without needing to construct their own fragment size ladder.

Flexible export formats

Added an export that allows users to format their data export without any programming. This allows users to export in multiple different formats for downstream use or processing. It allows users to choose the type and order of the data they are exporting and whether they want a row to be a sample, a locus, or a peak.

Simultaneous Mixed/Single Source Analysis

OSIRIS can apply the stutter filter, adenylation filter, fractional filter, and pull-up fractional filter differentially to single source samples, like knowns and references, and possibly mixed samples, like casework samples or chimerism study samples that are in the same analysis run. Sample type can be detected by matching character strings within the file or sample name. This can be particularly helpful when running reference and mixed samples, either to reduce the amount of editing of the reference samples or where the exported data will be used in mixture analysis software that

requires stutter peaks to be called. Added settings to specify either sample type as the default and allow character strings to identify the other sample type, simplifying use of this function.

Use of Non-Roman and Other Unicode Characters

OSIRIS now allows use of non-ASCII characters in file paths and filenames, so international users can use non-Roman and other Unicode characters in directory/folder and file names.

Identify Lab Settings Folders

OSIRIS now allows users to easily identify and find the location of Lab Settings folders. Clicking the folder icon button in the Lab Settings window will open the parent folder with the Lab Settings folder selected. This allows users to zip or compress the Lab Settings folder for easy exchange.

Bug Fixes

- Fixed the Mac version of OSIRIS so that windows open correctly with the latest version of the Mac OS Software. (Fixed in both 2.13 and 2.12.2.)
- Fixed a bug that could prevent analysis in RAPID-DNA samples that had high levels of noise.
- Fixed pull-up identification bugs that existed in previous versions that in rare circumstances might have prevented calling pullup but would not have prevented alleles from being called.
 - Fixed a bug that in rare circumstances prevented suspected pull-up crater side-peaks and sigmoidal peaks from being called as pull-up.
 - Fixed a bug in the pull-up algorithm that did not identify some pull-up peaks because the peaks were wider than expected.
 - Fixed a bug in the pull-up algorithm that failed to identify some spikes.
- Fixed a bug in the pull-up algorithm that incorrectly applied the spike artifact to some peaks that were not spikes.